SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Lee, James
                   Wood, William I.

   (ii) TITLE OF INVENTION: VEGF-Related Protein

  (iii) NUMBER OF SEQUENCES: 12

   (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Genentech, Inc.
        (B) STREET: 460 Point San Bruno Blvd
        (C) CITY: South San Francisco
        (D) STATE: California
        (E) COUNTRY: USA
        (F) ZIP: 94080

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: WinPatin (Genentech)

   (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

  (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: 60/003491
        (B) FILING DATE: 09/08/1995

 (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Lee, Wendy M.
        (B) REGISTRATION NUMBER: P-40,378
        (C) REFERENCE/DOCKET NUMBER: P0963R1

   (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 415/225-1994
        (B) TELEFAX: 415/952-9881
        (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2031 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGGGGTGT TCTGGTGTCC CCCGCCCCGC CTCTCCAAAA AGCTACACCG 50

ACGCGGACCG CGGCGGCGTC CTCCCTCGCC CTCGCTTCAC CTCGCGGGCT 100

CCGAATGCGG GGAGCTCGGA TGTCCGGTTT CCTGTGAGGC TTTTACCTGA 150

CACCCGCCGC CTTTCCCCGG CACTGGCTGG GAGGGCGCCC TGCAAAGTTG 200

GGAACGCGGA GCCCCGGACC CGCTCCCGCC GCCTCCGGCT CGCCCAGGGG 250

GGGTCGCCGG GAGGAGCCCG GGGGAGAGGG ACCAGGAGGG GCCCGCGGCC 300

TCGCAGGGGC GCCCGCGCCC CCACCCCTGC CCCCGCCAGC GGACCGGTCC 350

CCCACCCCCG GTCCTTCCAC CATGCACTTG CTGGGCTTCT TCTCTGTGGC 400

GTGTTCTCTG CTCGCCGCTG CGCTGCTCCC GGGTCCTCGC GAGGCGCCCG 450

CCGCCGCCGC CGCCTTCGAG TCCGGACTCG ACCTCTCGGA CGCGGAGCCC 500

GACGCGGGCG AGGCCACGGC TTATGCAAGC AAAGATCTGG AGGAGCAGTT 550

ACGGTCTGTG TCCAGTGTAG ATGAACTCAT GACTGTACTC TACCCAGAAT 600

ATTGGAAAAT GTACAAGTGT CAGCTAAGGA AAGGAGGCTG GCAACATAAC 650

AGAGAACAGG CCAACCTCAA CTCAAGGACA GAAGAGACTA TAAAATTTGC 700

TGCAGCACAT TATAATACAG AGATCTTGAA AAGTATTGAT AATGAGTGGA 750

GAAAGACTCA ATGCATGCCA CGGGAGGTGT GTATAGATGT GGGGAAGGAG 800

TTTGGAGTCG CGACAAACAC CTTCTTTAAA CCTCCATGTG TGTCCGTCTA 850

CAGATGTGGG GGTTGCTGCA ATAGTGAGGG GCTGCAGTGC ATGAACACCA 900

GCACGAGCTA CCTCAGCAAG ACGTTATTTG AAATTACAGT GCCTCTCTCT 950

CAAGGCCCCA AACCAGTAAC AATCAGTTTT GCCAATCACA CTTCCTGCCG 1000

ATGCATGTCT AAACTGGATG TTTACAGACA AGTTCATTCC ATTATTAGAC 1050

GTTCCCTGCC AGCAACACTA CCACAGTGTC AGGCAGCGAA CAAGACCTGC 1100

CCCACCAATT ACATGTGGAA TAATCACATC TGCAGATGCC TGGCTCAGGA 1150

AGATTTTATG TTTTCCTCGG ATGCTGGAGA TGACTCAACA GATGGATTCC 1200

ATGACATCTG TGGACCAAAC AAGGAGCTGG ATGAAGAGAC CTGTCAGTGT 1250

5   GTCTGCAGAG CGGGGCTTCG GCCTGCCAGC TGTGGACCCC ACAAAGAACT 1300

AGACAGAAAC TCATGCCAGT GTGTCTGTAA AAACAAACTC TTCCCCAGCC 1350

AATGTGGGGC CAACCGAGAA TTTGATGAAA ACACATGCCA GTGTGTATGT 1400

10

AAAAGAACCT GCCCCAGAAA TCAACCCCTA AATCCTGGAA AATGTGCCTG 1450

TGAATGTACA GAAAGTCCAC AGAAATGCTT GTTAAAAGGA AAGAAGTTCC 1500

15   ACCACCAAAC ATGCAGCTGT TACAGACGGC CATGTACGAA CCGCCAGAAG 1550

GCTTGTGAGC CAGGATTTTC ATATAGTGAA GAAGTGTGTC GTTGTGTCCC 1600

TTCATATTGG AAAAGACCAC AAATGAGCTA AGATTGTACT GTTTTCCAGT 1650

20   TCATCGATTT TCTATTATGG AAAACTGTGT TGCCACAGTA GAACTGTCTG 1700

TGAACAGAGA GACCCTTGTG GGTCCATGCT AACAAAGACA AAAGTCTGTC 1750

25   TTTCCTGAAC CATGTGGATA ACTTTACAGA AATGGACTGG AGCTCATCTG 1800

CAAAAGGCCT CTTGTAAAGA CTGGTTTTCT GCCAATGACC AAACAGCCAA 1850

GATTTTCCTC TTGTGATTTC TTTAAAAGAA TGACTATATA ATTTATTTCC 1900

30   ACTAAAAATA TTGTTTCTGC ATTCATTTTT ATAGCAACAA CAATTGGTAA 1950

AACTCACTGT GATCAATATT TTTATATCAT GCAAAATATG TTTAAAATAA 2000

35   AATGAAAATT GTATTAAAAA AAAAAAAAAA A 2031

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2031 base pairs
40   (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

45   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTTTTTT TTTTTAATA CAATTTTCAT TTTATTTTAA ACATATTTTG 50

50   CATGATATAA AAATATTGAT CACAGTGAGT TTTACCAATT GTTGTTGCTA 100

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TAAAAATGAA TGCAGAAACA ATATTTTTAG TGGAAATAAA TTATATAGTC 150
ATTCTTTTAA AGAAATCACA AGAGGAAAAT CTTGGCTGTT TGGTCATTGG 200
CAGAAAACCA GTCTTTACAA GAGGCCTTTT GCAGATGAGC TCCAGTCCAT 250
TTCTGTAAAG TTATCCACAT GGTTCAGGAA AGACAGACTT TTGTCTTTGT 300
TAGCATGGAC CCACAAGGGT CTCTCTGTTC ACAGACAGTT CTACTGTGGC 350
AACACAGTTT TCCATAATAG AAAATCGATG AACTGGAAAA CAGTACAATC 400
TTAGCTCATT TGTGGTCTTT TCCAATATGA AGGGACACAA CGACACACTT 450
CTTCACTATA TGAAAATCCT GGCTCACAAG CCTTCTGGCG GTTCGTACAT 500
GGCCGTCTGT AACAGCTGCA TGTTTGGTGG TGGAACTTCT TTCCTTTTAA 550
CAAGCATTTC TGTGGACTTT CTGTACATTC ACAGGCACAT TTTCCAGGAT 600
TTAGGGGTTG ATTTCTGGGG CAGGTTCTTT TACATACACA CTGGCATGTG 650
TTTTCATCAA ATTCTCGGTT GGCCCCACAT TGGCTGGGGA AGAGTTTGTT 700
TTTACAGACA CACTGGCATG AGTTTCTGTC TAGTTCTTTG TGGGGTCCAC 750
AGCTGGCAGG CCGAAGCCCC GCTCTGCAGA CACACTGACA GGTCTCTTCA 800
TCCAGCTCCT TGTTTGGTCC ACAGATGTCA TGGAATCCAT CTGTTGAGTC 850
ATCTCCAGCA TCCGAGGAAA ACATAAAATC TTCCTGAGCC AGGCATCTGC 900
AGATGTGATT ATTCCACATG TAATTGGTGG GGCAGGTCTT GTTCGCTGCC 950
TGACACTGTG GTAGTGTTGC TGGCAGGGAA CGTCTAATAA TGGAATGAAC 1000
TTGTCTGTAA ACATCCAGTT TAGACATGCA TCGGCAGGAA GTGTGATTGG 1050
CAAAACTGAT TGTTACTGGT TTGGGGCCTT GAGAGAGAGG CACTGTAATT 1100
TCAAATAACG TCTTGCTGAG GTAGCTCGTG CTGGTGTTCA TGCACTGCAG 1150
CCCCTCACTA TTGCAGCAAC CCCCACATCT GTAGACGGAC ACACATGGAG 1200
GTTTAAAGAA GGTGTTTGTC GCGACTCCAA ACTCCTTCCC CACATCTATA 1250
CACACCTCCC GTGGCATGCA TTGAGTCTTT CTCCACTCAT TATCAATACT 1300
TTTCAAGATC TCTGTATTAT AATGTGCTGC AGCAAATTTT ATAGTCTCTT 1350
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CTGTCCTTGA GTTGAGGTTG GCCTGTTCTC TGTTATGTTG CCAGCCTCCT 1400

TTCCTTAGCT GACACTTGTA CATTTTCCAA TATTCTGGGT AGAGTACAGT 1450

CATGAGTTCA TCTACACTGG ACACAGACCG TAACTGCTCC TCCAGATCTT 1500

TGCTTGCATA AGCCGTGGCC TCGCCCGCGT CGGGCTCCGC GTCCGAGAGG 1550

TCGAGTCCGG ACTCGAAGGC GGCGGCGGCG GCGGGCGCCT CGCGAGGACC 1600

CGGGAGCAGC ACAGCGGCGA GCAGAGAACA CGCCACAGAG AAGAAGCCCA 1650

GCAAGTGCAT GGTGGAAGGA CCGGGGGTGG GGGACCGGTC CGCTGGCGGG 1700

GGCAGGGGTG GGGGCGCGGG CGCCCCTGCG AGGCCGCGGG CCCCTCCTGG 1750

TCCCTCTCCC CCGGGCTCCT CCCGGCGACC CCCCCTGGGC GAGCCGGAGG 1800

CGGCGGGAGC GGGTCCGGGG CTCCGCGTTC CCAACTTTGC AGGGCGCCCT 1850

CCCAGCCAGT ACCGGGGAAA GGCGGCGGGT GTCAGGTAAA AGCCTCACAG 1900

GAAACCGGAC ATCCGAGCTC CCCGCATTCG GAGCCCGCGA GGTGAAGCGA 1950

GGGCGAGGGA GGACGCCGCC GCGGTCCGCG TCGGTGTAGC TTTTTGGAGA 2000

GGCGGGGCGG GGGACACCAG AACACCCCGC G 2031

(2) INFORMATION FOR SEQ ID NO:3:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 419 amino acids
      (B) TYPE: Amino Acid
      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala
  1   5   10   15

Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala
             20   25   30

Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
             35   40   45

Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
             50   55   60

Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
            65   70   75

Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
            80   85   90

Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
            95   100   105

Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
           110   115   120

Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
           125   130   135

Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
           140   145   150

Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
           155   160   165

Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr
           170   175   180

Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly
           185   190   195

Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
           200   205   210

Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
           215   220   225

Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
           230   235   240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg
           245   250   255

Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp
           260   265   270

Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu
           275   280   285

Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg
           290   295   300

Pro Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys
           305   310   315

Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala
                320   325   330

Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg
                335   340   345

Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys
                350   355   360

Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys
                365   370   375

Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn
                380   385   390

Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val
                395   400   405

Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met Ser
                410   415   419

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 147 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu
  1   5   10   15

Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala
                20   25   30

Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp
                35   40   45

Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
                50   55   60

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro
                65   70   75

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
                80   85   90

Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln
                95   100   105

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```
      Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met
                      110                 115                 120

      Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp
                      125                 130                 135

      Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg
                      140                 145     147
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 149 amino acids
       (B) TYPE: Amino Acid
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
      Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala
        1               5                  10                  15

      Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser
                       20                  25                  30

      Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu
                       35                  40                  45

      Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp
                       50                  55                  60

      Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro
                       65                  70                  75

      Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu
                       80                  85                  90

      Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Glu
                       95                 100                 105

      Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu
                      110                 115                 120

      Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu
                      125                 130                 135

      Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg
                      140                 145                 149
```

(2) INFORMATION FOR SEQ ID NO:6:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 299 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:


CCGTCTACAG ATGTGGGGGT TGCTGCAATA GTGAGGGGCT GCAGTGCATG 50

AACACCAGCA CGAGCTACCT CAGNAAGACG TTATTTGAAA TTACAGTGCC 100

TCTCTCTCAA GGCCCCAAAC CAGTAACAAT CAGTTTTGCC AATCACACTT 150

CCTGCCGATG CATGTCTAAA CTGGATGTTT ACAGACAAGT TCATTCCATT 200

ATTAGACGTT CCCTGCCAGC AACACTACCA CAGTGTCAGG CAGCGAACAA 250

GACCTGCCCC ACCAATTACA TGTGGAATAA TCACATCTGC AGATGCCTG 299
```

(2) INFORMATION FOR SEQ ID NO:7:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:


CTGGTGTTCA TGCACTGCAG CCCCTCACTA TTGCAGCAAC CCCCACATCT 50
```

(2) INFORMATION FOR SEQ ID NO:8:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:


GCATCTGCAG ATGTGATTAT TCCACATGTA ATTGGTGGGG CAGGTCTTGT 50
```

(2) INFORMATION FOR SEQ ID NO:9:

```
    (i) SEQUENCE CHARACTERISTICS:
```

```
        (A) LENGTH: 8 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

    Tyr Ser Met Thr Pro Pro Thr Leu
     1               5               8

(2) INFORMATION FOR SEQ ID NO:10:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

    Ser Leu Arg Arg Arg Gln Gln Gln Asp
     1               5                   9

(2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

    Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn
     1               5                   10                  15

    Arg Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln Leu Leu Glu
                    20                  25                  30

    Gly Gly Ala Ala His Tyr Ala Leu Leu Pro
                    35                  40

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

    Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu
     1               5                   10          13
```